Bacterial wilt resistance in tomato, eggplant and pepper: genetic resources challenged with the multifaceted *Ralstonia solanacearum* species complex

*Ralstonia solanacearum*
- causal agent of vascular diseases that cause severe economic losses,
- present in tropical and also temperate regions,
- unusual genetic and phenotypic diversity
- a species complex structured into 4 phylogenotypes.

**Host resistance**
- remains the most effective control strategy,
- resistance is often partially in solanaceous crops and quantitatively expressed,
- could be overcome by some *R. solanacearum* strains.

Varietal resistance properties vary according to geographical location due to the strong influence of environmental factors and the high genetic and phenotypic diversity of *R. solanacearum*.

**Objectives**
Re-investigate the resistance of solanaceous crops challenged with phylogenetically diverse strains of the *R. solanacearum* complex.

**Results**
- Six classes of phenotypic interaction:

  1. Highly resistant
  2. Moderately resistant
  3.1. Partially resistant
  3.2. Latent infection
  4. Moderately susceptible
  5. Highly susceptible

- Working definitions:
  **pathoprofile**: cluster of strains unified by a similar pattern of virulence on the Core-TEP;
  **pathotype**: cluster of strains unified by a similar pattern of virulence on one species [Tomato, eggplant or Pepper].
- The most aggressive strains belong to phylogroup I, IIB and III and were assigned to pathoprofiles d, e and f, and to pathotype tomato 4, pathotype eggplant 5 and pathotype pepper 3.
- The emerging strain from French West Indies CFP6783 [3] is the most virulent and aggressive strain: it attacks 26 out of 30 tested accessions and it causes more symptoms.

**References**

**Material & Methods**
- Core-TEP: 10 accessions of each species (Tomato, Eggplant and Pepper) among 24 lines are known for their resistance to Bacterial wilt;
- Core-Rs2: 12 strains virulent on three solanaceae, and representative of phylogroup I, II and III. The phylogroup IV is not considered in this study.
- Test in quarantine controlled environment (Rotoplan® NS2 or NS3);
- Inoculation by pouring 5ml of bacterial suspension (10⁸ CFU.mL⁻¹) after wounding lateral roots;
- Variables used for describing the disease:
  - % percentage of wilted plants,
  - colonization index [1,2] taking into account the rate of infected symptomless plant;
- Descriptive statistics analysis. The phenotypes were identified by fuzzy analysis clustering and agglomerative hierarchical nesting classification (euclidian distance and average linkage method) of R package cluster. The clusters of strains [pathoprofile/pathotype] were identified by agglomerative hierarchical nesting classification (euclidian distance and average linkage method).

**Conclusions & Perspectives**
- The three Solanaceae species present different mechanisms for resistance: partial, complete and latent infection.
- Neither pathotypes nor pathoprofiles were phylogroup-specific.
- The validation of pathotypes and pathoprofiles needs more data from naturally infested fields (ongoing works by breeding partners).
- A unique study that offered different models to further investigate interaction that results in compatible and incompatible pathosystems.